



PCT

RAW SEQUENCE LISTING

DATE: 04/03/2003

PATENT APPLICATION: US/10/070,982A

TIME: 11:52:13

Input Set : A:\FBRC011US.txt

Output Set: N:\CRF4\04032003\J070982A.raw

3 <110> APPLICANT: CAMINSCHI ET AL.
 5 <120> TITLE OF INVENTION: DENDRITIC CELL MEMBRANE PROTEIN FIRE
 7 <130> FILE REFERENCE: FBRC:011US
 9 <140> CURRENT APPLICATION NUMBER: 10/070,982A
 C--> 10 <141> **CURRENT FILING DATE: 2002-12-18**
 12 <150> PRIOR APPLICATION NUMBER: PCT/AU00/01083
 13 <151> PRIOR FILING DATE: 2000-09-11
 15 <160> NUMBER OF SEQ ID NOS: 25
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 681
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Mus musculus
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 29 20 25 30
 31 Cys Asn Glu Asn Ala Ser Cys Phe Asn Ser Thr His Cys Val Cys Lys
 32 35 40 45
 34 Glu Gly Phe Trp Thr Gly Ser Glu Asn Arg Arg Ile Ile Glu Pro His
 35 50 55 60
 37 Glu Lys Cys Gln Asp Ile Asn Glu Cys Leu Leu Lys Glu Leu Val Cys
 38 65 70 75 80
 40 Lys Asp Val Ser Tyr Cys Arg Asn Lys Ile Gly Thr Tyr Ile Cys Ser
 41 85 90 95
 43 Cys Val Val Lys Tyr Pro Leu Phe Asn Trp Val Ala Gly Ile Ile Asn
 44 100 105 110
 46 Ile Asp His Pro Asp Cys Tyr Val Asn Lys Ser Lys Asn Thr Gly Ser
 47 115 120 125
 49 Lys Thr His Thr Leu Gly Val Leu Ser Glu Phe Lys Ser Lys Glu Glu
 50 130 135 140
 52 Val Ala Lys Gly Ala Thr Lys Leu Leu Arg Lys Val Glu His His Ile
 53 145 150 155 160
 55 Leu Asn Glu Asn Ser Asp Ile Pro Lys Lys Asp Glu Asn Pro Leu Leu
 56 165 170 175
 58 Asp Ile Val Tyr Glu Thr Lys Arg Cys Lys Thr Met Thr Leu Leu Glu
 59 180 185 190
 61 Ala Gly Asn Asn Thr Met Lys Val Asp Cys Thr Ser Gly Phe Lys Glu
 62 195 200 205
 64 His Asn Ser Gly Gly Glu Thr Ala Val Ala Phe Ile Ala Tyr Lys Ser
 65 210 215 220
 67 Leu Gly Asn Leu Leu Asn Gly Ser Phe Phe Ser Asn Glu Glu Gly Phe

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70 Gln Glu Val Thr Leu Asn Ser His Ile Val Ser Gly Ala Ile Arg Ser
71          245          250          255
73 Glu Val Lys Pro Val Leu Ser Glu Pro Val Leu Leu Thr Leu Gln Asn
74          260          265          270
76 Ile Gln Pro Ile Asp Ser Arg Ala Glu His Leu Cys Val His Trp Glu
77          275          280          285
79 Gly Ser Glu Glu Gly Gly Ser Trp Ser Thr Lys Gly Cys Ser His Val
80          290          295          300
82 Tyr Thr Asn Asn Ser Tyr Thr Ile Cys Lys Cys Phe His Leu Ser Ser
83 305          310          315          320
85 Phe Ala Val Leu Met Ala Leu Pro His Glu Glu Asp Gly Val Leu Ser
86          325          330          335
88 Ala Leu Ser Val Ile Thr Tyr Val Gly Leu Ser Leu Ser Leu Leu Cys
89          340          345          350
91 Leu Phe Leu Ala Ala Ile Thr Phe Leu Leu Cys Arg Pro Ile Gln Asn
92          355          360          365
94 Thr Ser Thr Thr Leu His Leu Gln Leu Ser Ile Cys Leu Phe Leu Ala
95          370          375          380
97 Asp Leu Leu Phe Leu Thr Gly Ile Asn Arg Thr Lys Pro Lys Val Leu
98 385          390          395          400
100 Cys Ser Ile Ile Ala Gly Met Leu His Tyr Leu Tyr Leu Ala Ser Phe
101          405          410          415
103 Met Trp Met Phe Leu Glu Gly Leu His Leu Phe Leu Thr Val Ser Asn
104          420          425          430
106 Leu Lys Val Ala Asn Tyr Ser Asn Ser Gly Arg Phe Lys Lys Arg Phe
107          435          440          445
109 Met Tyr Pro Val Gly Tyr Gly Leu Pro Ala Phe Ile Val Ala Val Ser
110          450          455          460
112 Ala Ile Ala Gly His Lys Asn Tyr Gly Thr His Asn His Cys Trp Leu
113 465          470          475          480
115 Ser Leu His Arg Gly Phe Ile Trp Ser Phe Leu Gly Pro Ala Ala Ala
116          485          490          495
118 Ile Ile Leu Ile Asn Leu Val Phe Tyr Phe Leu Ile Ile Trp Ile Leu
119          500          505          510
121 Arg Ser Lys Leu Ser Ser Leu Asn Lys Glu Val Ser Thr Leu Gln Asp
122          515          520          525
124 Thr Lys Val Met Thr Phe Lys Ala Ile Val Gln Leu Phe Val Leu Gly
125          530          535          540
127 Cys Ser Trp Gly Ile Gly Leu Phe Ile Phe Ile Glu Val Gly Lys Thr
128 545          550          555          560
130 Val Arg Leu Ile Val Ala Tyr Leu Phe Thr Ile Ile Asn Val Leu Gln
131          565          570          575
133 Gly Val Leu Ile Phe Met Val His Cys Leu Leu Asn Arg Gln Val Arg
134          580          585          590
136 Met Glu Tyr Lys Lys Trp Phe His Arg Leu Arg Lys Glu Val Glu Ser
137          595          600          605
139 Glu Ser Thr Glu Val Ser His Ser Thr Thr His Thr Lys Met Gly Leu
140          610          615          620

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142 Ser Leu Asn Leu Glu Asn Phe Cys Pro Thr Gly Asn Leu His Asp Pro
143 625                               630                               635                               640
145 Ser Asp Ser Ile Leu Pro Ser Thr Glu Val Ala Gly Val Tyr Leu Ser
146                               645                               650                               655
148 Thr Pro Arg Ser His Met Gly Ala Glu Asp Val Asn Ser Gly Thr His
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151 Ala Tyr Trp Ser Arg Thr Ile Ser Asp
152                               675                               680
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156 <211> LENGTH: 635
157 <212> TYPE: PRT
158 <213> ORGANISM: Homo sapiens
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167 Phe His Asp Ser Ser Glu Lys Cys Glu Asp Ile Asn Glu Cys Glu Thr
168                               35                               40                               45
170 Gly Leu Ala Lys Cys Lys Tyr Lys Ala Tyr Cys Arg Asn Lys Val Gly
171                               50                               55                               60
173 Gly Tyr Ile Cys Ser Cys Leu Val Lys Tyr Thr Leu Phe Asn Phe Leu
174 65                               70                               75                               80
176 Ala Gly Ile Ile Asp Tyr Asp His Pro Asp Cys Tyr Glu Asn Asn Ser
177                               85                               90                               95
179 Gln Gly Thr Thr Gln Ser Asn Val Asp Ile Trp Glu Asn Leu Arg Arg
180                               100                              105                              110
182 Asn Gly Ser Arg Glu Asp Phe Ala Arg Arg Ala Thr Gln Leu Ile Gln
183                               115                              120                              125
185 Ser Val Glu Leu Ser Ile Trp Asn Ala Ser Phe Ala Ser Pro Gly Lys
186                               130                              135                              140
188 Gly Gln Ile Ser Glu Phe Asp Ile Val Tyr Glu Thr Lys Arg Cys Asn
189 145                              150                              155                              160
191 Glu Thr Arg Glu Asn Ala Phe Leu Glu Ala Gly Asn Asn Thr Met Asp
192                               165                              170                              175
194 Ile Asn Cys Ala Asp Ala Leu Lys Gly Asn Leu Arg Glu Ser Thr Ala
195                               180                              185                              190
197 Val Ala Leu Ile Thr Tyr Gln Ser Leu Gly Asp Ile Leu Asn Ala Ser
198                               195                              200                              205
200 Phe Phe Ser Lys Arg Lys Gly Met Gln Glu Val Lys Leu Asn Ser Tyr
201                               210                              215                              220
203 Val Val Ser Gly Thr Val Gly Leu Lys Glu Lys Ile Ser Leu Ser Glu
204 225                              230                              235                              240
206 Pro Val Phe Leu Thr Phe Arg His Asn Gln Pro Gly Asp Lys Arg Thr
207                               245                              250                              255
209 Lys His Ile Cys Val Tyr Trp Glu Gly Ser Glu Gly Gly Arg Trp Ser
210                               260                              265                              270
212 Thr Glu Gly Cys Ser His Val His Ser Asn Gly Ser Tyr Thr Lys Cys
213                               275                              280                              285

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215 Lys Cys Phe His Leu Ser Ser Phe Ala Val Leu Val Ala Leu Ala Pro
216      290      295      300
218 Lys Glu Asp Pro Val Leu Thr Val Ile Thr Gln Val Gly Leu Thr Ile
219 305      310      315      320
221 Ser Leu Leu Cys Leu Phe Leu Ala Ile Leu Thr Phe Leu Leu Cys Arg
222      325      330      335
224 Pro Ile Gln Asn Thr Ser Thr Ser Leu His Leu Glu Leu Ser Leu Cys
225      340      345      350
227 Leu Phe Leu Ala His Leu Leu Phe Leu Thr Gly Ile Asn Arg Thr Glu
228      355      360      365
230 Pro Glu Val Leu Cys Ser Ile Ile Ala Gly Leu Leu His Phe Leu Tyr
231      370      375      380
233 Leu Ala Cys Phe Thr Trp Met Leu Leu Glu Gly Leu His Leu Phe Leu
234 385      390      395      400
236 Thr Val Arg Asn Leu Lys Val Ala Asn Tyr Thr Ser Thr Gly Arg Phe
237      405      410      415
239 Lys Lys Arg Phe Met Tyr Pro Val Gly Tyr Gly Ile Pro Ala Val Ile
240      420      425      430
242 Ile Ala Val Ser Ala Ile Val Gly Pro Gln Asn Tyr Gly Thr Phe Thr
243      435      440      445
245 His Cys Trp Leu Lys Leu Asp Lys Gly Phe Ile Trp Ser Phe Met Gly
246      450      455      460
248 Pro Val Ala Val Ile Ile Leu Ile Asn Leu Val Phe Tyr Phe Gln Val
249 465      470      475      480
251 Leu Trp Ile Leu Arg Ser Lys Leu Ser Ser Leu Asn Lys Glu Val Ser
252      485      490      495
254 Thr Ile Gln Asp Thr Arg Val Met Thr Phe Lys Ala Ile Ser Gln Leu
255      500      505      510
257 Phe Ile Leu Gly Cys Ser Trp Gly Leu Gly Phe Phe Met Val Glu Glu
258      515      520      525
260 Val Gly Lys Thr Ile Gly Ser Ile Ile Ala Tyr Ser Phe Thr Ile Ile
261      530      535      540
263 Asn Thr Leu Gln Gly Val Leu Leu Phe Val Val His Cys Leu Leu Asn
264 545      550      555      560
266 Arg Gln Val Arg Met Glu Tyr Lys Lys Trp Phe Ser Gly Met Arg Lys
267      565      570      575
269 Gly Val Glu Thr Glu Ser Thr Glu Met Ser Arg Ser Thr Thr Gln Thr
270      580      585      590
272 Lys Thr Glu Glu Val Gly Lys Ser Ser Glu Ile Phe His Lys Gly Gly
273      595      600      605
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276      610      615      620
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279 625      630      635
281 <210> SEQ ID NO: 3
282 <211> LENGTH: 3258
283 <212> TYPE: DNA
284 <213> ORGANISM: Mus musculus
286 <400> SEQUENCE: 3

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287 accactgctt cattgctgct gagaatgttc caggctgagt gagaagtaaa aattcatcat 60
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289 tagagatatg ggaagcaggt gccttctgca tgcctcagtt cctggaatgc tgcttatctg 180
290 gtcaatatta caaatgatga atatttcagc ttctgtccc cagtgaatg aaaatgccag 240
291 ctgcttcaac agcaccact gtgtttgtaa agaaggattc tggacgggct ctgagaatag 300
292 aagaattatt gagcccatg agaaatgtca agatattaat gagtgtctac tgaaagaatt 360
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299 gaaggttgac tgcactagt gtttcaaaga gcacaacagt ggaggtgaaa ctgcagtggc 780
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VERIFICATION SUMMARY

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